Toshihide Ueno

List of Publications by Year
in descending order

35 papers	1,763 citations	361413 20 h-index	377865 34 g-index
36 all docs	36 docs citations	36 times ranked	4190 citing authors

#	Article	IF	Citations
1	PD-1 blockade therapy promotes infiltration of tumor-attacking exhausted TÂcell clonotypes. Cell Reports, 2022, 38, 110331.	6.4	45
2	Transcriptomic Profiling of MSI-H/dMMR Gastrointestinal Tumors to Identify Determinants of Responsiveness to Antiâ€"PD-1 Therapy. Clinical Cancer Research, 2022, 28, 2110-2117.	7.0	30
3	Comparative Study on the Efficacy and Exposure of Molecular Target Agents in Nonâ€"small Cell Lung Cancer PDX Models with Driver Genetic Alterations. Molecular Cancer Therapeutics, 2022, 21, 359-370.	4.1	3
4	A Low Tumor Mutational Burden and *PTEN* Mutations Are Predictors of a Negative Response to PD-1 Blockade in MSI-H/dMMR Gastrointestinal Tumors. Clinical Cancer Research, 2021, 27, 3714-3724.	7.0	61
5	Comprehensive functional evaluation of variants of fibroblast growth factor receptor genes in cancer. Npj Precision Oncology, 2021, 5, 66.	5.4	19
6	Multi-omic profiling of peritoneal metastases in gastric cancer identifies molecular subtypes and therapeutic vulnerabilities. Nature Cancer, 2021, 2, 962-977.	13.2	41
7	Transcript-targeted analysis reveals isoform alterations and double-hop fusions in breast cancer. Communications Biology, 2021, 4, 1320.	4.4	13
8	MicroSEC filters sequence errors for formalin-fixed and paraffin-embedded samples. Communications Biology, 2021, 4, 1396.	4.4	2
9	A Hyperactive RelA/p65-Hexokinase 2 Signaling Axis Drives Primary Central Nervous System Lymphoma. Cancer Research, 2020, 80, 5330-5343.	0.9	19
10	Assessment of Predictive Biomarkers of the Response to Pazopanib Based on an Integrative Analysis of High-grade Soft-tissue Sarcomas: Analysis of a Tumor Sample from a Responder and Patients with Other Soft-tissue Sarcomas. Clinical Orthopaedics and Related Research, 2020, 478, 2461-2476.	1.5	9
11	Targeting MEF2D-fusion Oncogenic Transcriptional Circuitries in B-cell Precursor Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 82-95.	5.0	12
12	An Oncogenic Alteration Creates a Microenvironment that Promotes Tumor Progression by Conferring a Metabolic Advantage to Regulatory T Cells. Immunity, 2020, 53, 187-203.e8.	14.3	119
13	High-throughput functional evaluation of BRCA2 variants of unknown significance. Nature Communications, 2020, 11, 2573.	12.8	38
14	Targeting MEF2D-fusion Oncogenic Transcriptional Circuitries in B-cell Precursor Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 82-95.	5.0	0
15	Genomic profiles of colorectal carcinoma with liver metastases and newly identified fusion genes. Cancer Science, 2019, 110, 2973-2981.	3.9	23
16	Identification of candidates for driver oncogenes in scirrhousâ€type gastric cancer cell lines. Cancer Science, 2019, 110, 2643-2651.	3.9	8
17	A germline HLTF mutation in familial MDS induces DNA damage accumulation through impaired PCNA polyubiquitination. Leukemia, 2019, 33, 1773-1782.	7.2	11
18	Uterine adenomyosis is an oligoclonal disorder associated with KRAS mutations. Nature Communications, 2019, 10, 5785.	12.8	82

#	Article	IF	Citations
19	Fusion Kinases Identified by Genomic Analyses of Sporadic Microsatellite Instability–High Colorectal Cancers. Clinical Cancer Research, 2019, 25, 378-389.	7.0	49
20	Pediatric soft tissue tumor of the upper arm with LMNA-NTRK1 fusion. Human Pathology, 2018, 72, 167-173.	2.0	13
21	Transcriptional activities of DUX4 fusions in B-cell acute lymphoblastic leukemia. Haematologica, 2018, 103, e522-e526.	3.5	17
22	High-Throughput Functional Evaluation of Variants of Unknown Significance in *ERBB2*. Clinical Cancer Research, 2018, 24, 5112-5122.	7.0	60
23	Genome-wide CRISPR screen identifies *TMEM41B* as a gene required for autophagosome formation. Journal of Cell Biology, 2018, 217, 3817-3828.	5.2	168
24	Inactivating mutations and hypermethylation of the *NKX2‐1/TTF‐1* gene in non‐terminal respiratory unit‐type lung adenocarcinomas. Cancer Science, 2017, 108, 1888-1896.	3.9	28
25	A method of high-throughput functional evaluation of *EGFR* gene variants of unknown significance in cancer. Science Translational Medicine, 2017, 9, .	12.4	168
26	Integrative analysis of genomic alterations in triple-negative breast cancer in association with homologous recombination deficiency. PLoS Genetics, 2017, 13, e1006853.	3.5	39
27	Genomic characterization of primary central nervous system lymphoma. Acta Neuropathologica, 2016, 131, 865-875.	7.7	138
28	Micro RNA‐31 is a positive modulator of endothelial–mesenchymal transition and associated secretory phenotype induced by TGF‐β. Genes To Cells, 2016, 21, 99-116.	1.2	46
29	Recurrent DUX4 fusions in B cell acute lymphoblastic leukemia of adolescents and young adults. Nature Genetics, 2016, 48, 569-574.	21.4	198
30	Mutational Landscape and Antiproliferative Functions of ELF Transcription Factors in Human Cancer. Cancer Research, 2016, 76, 1814-1824.	0.9	31
31	Transforming somatic mutations of mammalian target of rapamycin kinase in human cancer. Cancer Science, 2015, 106, 1687-1692.	3.9	18
32	Oncogenic activity of BIRC2 and BIRC3 mutants independent of nuclear factor‐κB‐activating potential. Cancer Science, 2015, 106, 1137-1142.	3.9	24
33	miR-378a-3p modulates tamoxifen sensitivity in breast cancer MCF-7 cells through targeting GOLT1A. Scientific Reports, 2015, 5, 13170.	3.3	82
34	Small-RNA asymmetry is directly driven by mammalian Argonautes. Nature Structural and Molecular Biology, 2015, 22, 512-521.	8.2	75
35	Recurrent CDC25C mutations drive malignant transformation in FPD/AML. Nature Communications, 2014, 5, 4770.	12.8	74